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**HAND CARRY TO:
Special Programs Examiner Tsang
Crystal Mall 1, 7th Floor
Patent & Trademark Office
1911 South Clark Place
Arlington, VA 22202**

In re International Patent Application of

DUKE UNIVERSITY ET AL

Agent's File Ref: 1579-379

International Application No: **PCT/US99/17678**
International Filing Date: 05 August 1999

For: URATE OXIDASE

15 February 2000

United States Receiving Office
Honorable Commissioner of Patents
and Trademarks
Washington, D.C. 20231

Response to Telephonic Request

Dear Sirs,

Responsive to Examiner Tsang's telephonic request of February 15, 2000, made to the undersigned, attached is a further paper and computer readable copy of the Sequence Listing filed November 19, 1999, along with a copy of the Applicants' Response of November 19, 1999 and date stamped post card Receipt from the submission of November 19, 1999.

In accordance with 37 CFR 1.821-1.825, I hereby state that the content of the paper and computer-readable copies of the sequence listing submitted in accordance with 37 CFR 1.821(c) and (e), respectively, are the same. I hereby state that the submission, filed in accordance with 37 CFR 1.821(g), does not introduce new matter.

The Examiner is requested to contact the undersigned if anything further is required. A Search of all of the claims is requested.

Respectfully submitted,

NIXON & VANDERHYE P.C.



B. J. Sadoff

Reg No 3666

8th Floor
1100 North Glebe Road
Arlington, Virginia 22201-4714

SEQUENCE LISTING

<110> HERSHFIELD, MICHAEL S.
KELLY, SUSAN J.

<120> URATE OXIDASE

<130> 1579-379

<140> PCT/US99/17678

<141> 1999-08-05

<160>11

<170> PatentIn Ver. 2.0

<210> 1

<211> 915

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(915)

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20 25 30	
cga gat gga aaa tat cac agc att aaa gag gtg gca act tca gtg caa	144
Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln	
35 40 45	
ctg act ttg agc tcc aaa aaa gat tac ctg cat gga gac aat tca gat	192
Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp	
50 55 60	
gtc atc cct aca gac acc atc aag aac aca gtt aat gtc ctg gcg aag	240
Val Ile Pro Thr Asp Thr Ile Lys Asn Thr Val Asn Val Leu Ala Lys	
65 70 75 80	
ttc aaa ggc atc aaa agc ata gaa act ttt gct gtg act atc tgt gag	288
Phe Lys Gly Ile Lys Ser Ile Glu Thr Phe Ala Val Thr Ile Cys Glu	
85 90 95	
cat ttc ctt tct tcc ttc aag cat gtc atc aga gct caa gtc tat gtg	336
His Phe Leu Ser Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val	
100 105 110	
gaa gaa gtt cct tgg aag cgt ttt gaa aag aat gga gtt aag cat gtc	384
Glu Glu Val Pro Trp Lys Arg Phe Glu Lys Asn Gly Val Lys His Val	
115 120 125	
cat gca ttt att tat act cct act gga acg cac ttc tgt gag gtt gaa	432
His Ala Phe Ile Tyr Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu	
130 135 140	
cag ata agg aat gga cct cca gtc att cat tct gga atc aaa gac cta	480

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Lys	Val	Leu	Lys	Thr	Thr	Gln	Ser	Gly	Phe	Glu	Gly	Phe	Ile	Lys	Asp	
				165					170					175		
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Gln	Phe	Thr	Thr	Leu	Pro	Glu	Val	Lys	Asp	Arg	Cys	Phe	Ala	Thr	Gln	
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gcc	acc	tgg	gac	act	gtt	agg	agc	att	gtc	ctg	cag	aaa	ttt	gct	ggg	672
Ala	Thr	Trp	Asp	Thr	Val	Arg	Ser	Ile	Val	Leu	Gln	Lys	Phe	Ala	Gly	
	210					215					220					
ccc	tat	gac	aaa	ggc	gag	tac	tca	ccc	tct	gtg	cag	aag	acc	ctc	tat	720
Pro	Tyr	Asp	Lys	Gly	Glu	Tyr	Ser	Pro	Ser	Val	Gln	Lys	Thr	Leu	Tyr	
225					230					235				240		
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Asp	Ile	Gln	Val	Leu	Ser	Leu	Ser	Arg	Val	Pro	Glu	Ile	Glu	Asp	Met	
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gaa	atc	agc	ctg	cca	aac	att	cac	tac	ttc	aat	ata	gac	atg	tcc	aaa	816
Glu	Ile	Ser	Leu	Pro	Asn	Ile	His	Tyr	Phe	Asn	Ile	Asp	Met	Ser	Lys	
			260					265					270			
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Met	Gly	Leu	Ile	Asn	Lys	Glu	Glu	Val	Leu	Leu	Pro	Leu	Asp	Asn	Pro	
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tga																915
305																

<210> 2

<211> 304

<212> PRT

<213> Artificial Sequence

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Arg	Asp	Gly	Lys	Tyr	His	Ser	Ile	Lys	Glu	Val	Ala	Thr	Ser	Val	Gln
		35					40					45			

Leu	Thr	Leu	Ser	Ser	Lys	Lys	Asp	Tyr	Leu	His	Gly	Asp	Asn	Ser	Asp
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Val	Ile	Pro	Thr	Asp	Thr	Ile	Lys	Asn	Thr	Val	Asn	Val	Leu	Ala	Lys
	65				70					75					80

Phe Lys Gly Ile Lys Ser Ile Glu Thr Phe Ala Val Thr Ile Cys Glu

85

90

95

His Phe Leu Ser Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val
 100 105 110
 Glu Glu Val Pro Trp Lys Arg Phe Glu Lys Asn Gly Val Lys His Val
 115 120 125
 His Ala Phe Ile Tyr Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu
 130 135 140
 Gln Ile Arg Asn Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu
 145 150 155 160
 Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp
 165 170 175
 Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln
 180 185 190
 Val Tyr Cys Lys Trp Arg Tyr His Gln Gly Arg Asp Val Asp Phe Glu
 195 200 205
 Ala Thr Trp Asp Thr Val Arg Ser Ile Val Leu Gln Lys Phe Ala Gly
 210 215 220
 Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr
 225 230 235 240
 Asp Ile Gln Val Leu Ser Leu Ser Arg Val Pro Glu Ile Glu Asp Met
 245 250 255
 Glu Ile Ser Leu Pro Asn Ile His Tyr Phe Asn Ile Asp Met Ser Lys
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 Tyr Gly Lys Ile Thr Gly Thr Val Lys Arg Lys Leu Ser Ser Arg Leu
 290 295 300

<210> 3

<211> 915

<212> DNA

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<221> CDS

<222> (1)..(915)

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<223> Description of Artificial Sequence:pks chimera

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gtc cga act ggc tat ggg aag gat atg ata aaa gtt ctc cat att cag 96
 Val Arg Thr Gly Tyr Gly Lys Asp Met Ile Lys Val Leu His Ile Gln
 20 25 30

cga gat gga aaa tat cac agc att aaa gag gtg gca act tca gtg caa 144
 Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln
 35 40 45

ctg act ttg agc tcc aaa aaa gat tac ctg cat gga gac aat tca gat	192
Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp	
50 55 60	
gtc atc cct aca gac acc atc aag aac aca gtt aat gtc ctg gcg aag	240
Val Ile Pro Thr Asp Thr Ile Lys Asn Thr Val Asn Val Leu Ala Lys	
65 70 75 80	
ttc aaa ggc atc aaa agc ata gaa act ttt gct gtg act atc tgt gag	288
Phe Lys Gly Ile Lys Ser Ile Glu Thr Phe Ala Val Thr Ile Cys Glu	
85 90 95	
cat ttc ctt tct tcc ttc aag cat gtc atc aga gct caa gtc tat gtg	336
His Phe Leu Ser Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val	
100 105 110	
gaa gaa gtt cct tgg aag cgt ttt gaa aag aat gga gtt aag cat gtc	384
Glu Glu Val Pro Trp Lys Arg Phe Glu Lys Asn Gly Val Lys His Val	
115 120 125	
cat gca ttt att tat act cct act gga acg cac ttc tgt gag gtt gaa	432
His Ala Phe Ile Tyr Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu	
130 135 140	
cag ata agg aat gga cct cca gtc att cat tct gga atc aaa gac cta	480
Gln Ile Arg Asn Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu	
145 150 155 160	
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Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp	
165 170 175	
cag ttc acc acc ctc cct gag gtg aag gac cgg tgc ttt gcc acc caa	576
Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln	
180 185 190	
gtg tac tgc aaa tgg cgc tac cac cag ggc aga gat gtg gac ttt gag	624
Val Tyr Cys Lys Trp Arg Tyr His Gln Gly Arg Asp Val Asp Phe Glu	
195 200 205	
gcc acc tgg gac act gtt agg agc att gtc ctg cag aaa ttt gct ggg	672
Ala Thr Trp Asp Thr Val Arg Ser Ile Val Leu Gln Lys Phe Ala Gly	
210 215 220	
ccc tat gac aaa ggc gag tac tcg ccc tct gtc cag aag aca ctc tat	720
Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr	
225 230 235 240	
gac atc cag gtg ctc acc ctg ggc cag gtt cct gag ata gaa gat atg	768
Asp Ile Gln Val Leu Thr Leu Gly Gln Val Pro Glu Ile Glu Asp Met	
245 250 255	
gaa atc agc ctg cca aat att cac tac tta aac ata gac atg tcc aaa	816
Glu Ile Ser Leu Pro Asn Ile His Tyr Leu Asn Ile Asp Met Ser Lys	
260 265 270	
atg gga ctg atc aac aag gaa gag gtc ttg cta cct tta gac aat cca	864
Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro	
275 280 285	
tat gga aaa att act ggt aca gtc aag agg aag ttg tct tca aga ctg	912
Tyr Gly Lys Ile Thr Gly Thr Val Lys Arg Lys Leu Ser Ser Arg Leu	
290 295 300	
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305

<210> 4

<211> 304

<212> PRT

<213> Artificial Sequence

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			20					25					30		
Arg	Asp	Gly	Lys	Tyr	His	Ser	Ile	Lys	Glu	Val	Ala	Thr	Ser	Val	Gln
		35					40				45				
Leu	Thr	Leu	Ser	Ser	Lys	Lys	Asp	Tyr	Leu	His	Gly	Asp	Asn	Ser	Asp
	50					55					60				
Val	Ile	Pro	Thr	Asp	Thr	Ile	Lys	Asn	Thr	Val	Asn	Val	Leu	Ala	Lys
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Phe	Lys	Gly	Ile	Lys	Ser	Ile	Glu	Thr	Phe	Ala	Val	Thr	Ile	Cys	Glu
				85					90					95	
His	Phe	Leu	Ser	Ser	Phe	Lys	His	Val	Ile	Arg	Ala	Gln	Val	Tyr	Val
			100					105					110		
Glu	Glu	Val	Pro	Trp	Lys	Arg	Phe	Glu	Lys	Asn	Gly	Val	Lys	His	Val
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His	Ala	Phe	Ile	Tyr	Thr	Pro	Thr	Gly	Thr	His	Phe	Cys	Glu	Val	Glu
	130					135					140				
Gln	Ile	Arg	Asn	Gly	Pro	Pro	Val	Ile	His	Ser	Gly	Ile	Lys	Asp	Leu
145					150					155					160
Lys	Val	Leu	Lys	Thr	Thr	Gln	Ser	Gly	Phe	Glu	Gly	Phe	Ile	Lys	Asp
				165					170					175	
Gln	Phe	Thr	Thr	Leu	Pro	Glu	Val	Lys	Asp	Arg	Cys	Phe	Ala	Thr	Gln
			180					185					190		
Val	Tyr	Cys	Lys	Trp	Arg	Tyr	His	Gln	Gly	Arg	Asp	Val	Asp	Phe	Glu
		195					200					205			
Ala	Thr	Trp	Asp	Thr	Val	Arg	Ser	Ile	Val	Leu	Gln	Lys	Phe	Ala	Gly
	210					215					220				
Pro	Tyr	Asp	Lys	Gly	Glu	Tyr	Ser	Pro	Ser	Val	Gln	Lys	Thr	Leu	Tyr
225					230					235				240	
Asp	Ile	Gln	Val	Leu	Thr	Leu	Gly	Gln	Val	Pro	Glu	Ile	Glu	Asp	Met
				245					250					255	
Glu	Ile	Ser	Leu	Pro	Asn	Ile	His	Tyr	Leu	Asn	Ile	Asp	Met	Ser	Lys
			260					265					270		
Met	Gly	Leu	Ile	Asn	Lys	Glu	Glu	Val	Leu	Leu	Pro	Leu	Asp	Asn	Pro
		275					280					285			
Tyr	Gly	Lys	Ile	Thr	Gly	Thr	Val	Lys	Arg	Lys	Leu	Ser	Ser	Arg	Leu
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<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: baboon D3H

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35 40 45
Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp
50 55 60
Ile Ile Pro Thr Asp Thr Ile Lys Asn Thr Val His Val Leu Ala Lys
65 70 75 80
Phe Lys Gly Ile Lys Ser Ile Glu Ala Phe Gly Val Asn Ile Cys Glu
85 90 95
Tyr Phe Leu Ser Ser Phe Asn His Val Ile Arg Ala Gln Val Tyr Val
100 105 110
Glu Glu Ile Pro Trp Lys Arg Leu Glu Lys Asn Gly Val Lys His Val
115 120 125
His Ala Phe Ile His Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu
130 135 140
Gln Leu Arg Ser Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu
145 150 155 160
Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp
165 170 175
Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln
180 185 190
Val Tyr Cys Lys Trp Arg Tyr His Gln Cys Arg Asp Val Asp Phe Glu
195 200 205
Ala Thr Trp Gly Thr Ile Arg Asp Leu Val Leu Glu Lys Phe Ala Gly
210 215 220
Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr
225 230 235 240
Asp Ile Gln Val Leu Ser Leu Ser Arg Val Pro Glu Ile Glu Asp Met
245 250 255
Glu Ile Ser Leu Pro Asn Ile His Tyr Phe Asn Ile Asp Met Ser Lys
260 265 270
Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro
275 280 285
Tyr Gly Lys Ile Thr Gly Thr Val Lys Arg Lys Leu Ser Ser Arg Leu

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			20					25					30		
Arg	Asp	Gly	Lys	Tyr	His	Ser	Ile	Lys	Glu	Val	Ala	Thr	Ser	Val	Gln
		35					40					45			
Leu	Thr	Leu	Ser	Ser	Lys	Lys	Asp	Tyr	Leu	His	Gly	Asp	Asn	Ser	Asp
	50					55					60				
Ile	Ile	Pro	Thr	Asp	Thr	Ile	Lys	Asn	Thr	Val	His	Val	Leu	Ala	Lys
	65				70					75					80
Phe	Lys	Gly	Ile	Lys	Ser	Ile	Glu	Ala	Phe	Gly	Val	Asn	Ile	Cys	Glu
				85					90					95	
Tyr	Phe	Leu	Ser	Ser	Phe	Asn	His	Val	Ile	Arg	Ala	Gln	Val	Tyr	Val
			100					105					110		
Glu	Glu	Ile	Pro	Trp	Lys	Arg	Leu	Glu	Lys	Asn	Gly	Val	Lys	His	Val
		115					120					125			
His	Ala	Phe	Ile	His	Thr	Pro	Thr	Gly	Thr	His	Phe	Cys	Glu	Val	Glu
	130					135					140				
Gln	Leu	Arg	Ser	Gly	Pro	Pro	Val	Ile	His	Ser	Gly	Ile	Lys	Asp	Leu
	145				150					155					160
Lys	Val	Leu	Lys	Thr	Thr	Gln	Ser	Gly	Phe	Glu	Gly	Phe	Ile	Lys	Asp
				165					170					175	
Gln	Phe	Thr	Thr	Leu	Pro	Glu	Val	Lys	Asp	Arg	Cys	Phe	Ala	Thr	Gln
			180					185					190		
Val	Tyr	Cys	Lys	Trp	Arg	Tyr	His	Gln	Cys	Arg	Asp	Val	Asp	Phe	Glu
		195					200					205			
Ala	Thr	Trp	Gly	Thr	Ile	Arg	Asp	Leu	Val	Leu	Glu	Lys	Phe	Ala	Gly
	210					215					220				
Pro	Tyr	Asp	Lys	Gly	Glu	Tyr	Ser	Pro	Ser	Val	Gln	Lys	Thr	Leu	Tyr
	225				230					235					240
Asp	Ile	Gln	Val	Leu	Ser	Leu	Ser	Arg	Val	Pro	Glu	Ile	Glu	Asp	Met
				245					250					255	
Glu	Ile	Ser	Leu	Pro	Asn	Ile	His	Tyr	Phe	Asn	Ile	Asp	Met	Ser	Lys
			260					265					270		
Met	Gly	Leu	Ile	Asn	Lys	Glu	Glu	Val	Leu	Leu	Pro	Leu	Asp	Asn	Pro
		275					280						285		

Tyr Gly Lys Ile Thr Gly Thr Val Lys Arg Lys Leu Ser Ser Arg Leu
 290 295 300

<210> 7
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 <212> PRT
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<400> 7

Met Ala His Tyr Arg Asn Asp Tyr Lys Lys Asn Asp Glu Val Glu Phe
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 Val Arg Thr Gly Tyr Gly Lys Asp Met Ile Lys Val Leu His Ile Gln
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 Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln
 35 40 45
 Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp
 50 55 60
 Val Ile Pro Thr Asp Thr Ile Lys Asn Thr Val Asn Val Leu Ala Lys
 65 70 75 80
 Phe Lys Gly Ile Lys Ser Ile Glu Thr Phe Ala Val Thr Ile Cys Glu
 85 90 95
 His Phe Leu Ser Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val
 100 105 110
 Glu Glu Val Pro Trp Lys Arg Phe Glu Lys Asn Gly Val Lys His Val
 115 120 125
 His Ala Phe Ile Tyr Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu
 130 135 140
 Gln Ile Arg Asn Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu
 145 150 155 160
 Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp
 165 170 175
 Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln
 180 185 190
 Val Tyr Cys Lys Trp Arg Tyr His Gln Gly Arg Asp Val Asp Phe Glu
 195 200 205
 Ala Thr Trp Asp Thr Val Arg Ser Ile Val Leu Gln Lys Phe Ala Gly
 210 215 220
 Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr
 225 230 235 240
 Asp Ile Gln Val Leu Thr Leu Gly Gln Val Pro Glu Ile Glu Asp Met
 245 250 255
 Glu Ile Ser Leu Pro Asn Ile His Tyr Leu Asn Ile Asp Met Ser Lys
 260 265 270
 Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro
 275 280 285

Tyr Gly Arg Ile Thr Gly Thr Val Lys Arg Lys Leu Thr Ser Arg Leu
 290 295 300

<210> 8
 <211> 298
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PBC amino truncated

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 20 25 30
 Ser Ile Lys Glu Val Ala Thr Ser Val Gln Leu Thr Leu Ser Ser Lys
 35 40 45
 Lys Asp Tyr Leu His Gly Asp Asn Ser Asp Val Ile Pro Thr Asp Thr
 50 55 60
 Ile Lys Asn Thr Val Asn Val Leu Ala Lys Phe Lys Gly Ile Lys Ser
 65 70 75 80
 Ile Glu Thr Phe Ala Val Thr Ile Cys Glu His Phe Leu Ser Ser Phe
 85 90 95
 Lys His Val Ile Arg Ala Gln Val Tyr Val Glu Glu Val Pro Trp Lys
 100 105 110
 Arg Phe Glu Lys Asn Gly Val Lys His Val His Ala Phe Ile Tyr Thr
 115 120 125
 Pro Thr Gly Thr His Phe Cys Glu Val Glu Gln Ile Arg Asn Gly Pro
 130 135 140
 Pro Val Ile His Ser Gly Ile Lys Asp Leu Lys Val Leu Lys Thr Thr
 145 150 155 160
 Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp Gln Phe Thr Thr Leu Pro
 165 170 175
 Glu Val Lys Asp Arg Cys Phe Ala Thr Gln Val Tyr Cys Lys Trp Arg
 180 185 190
 Tyr His Gln Gly Arg Asp Val Asp Phe Glu Ala Thr Trp Asp Thr Val
 195 200 205
 Arg Ser Ile Val Leu Gln Lys Phe Ala Gly Pro Tyr Asp Lys Gly Glu
 210 215 220
 Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr Asp Ile Gln Val Leu Ser
 225 230 235 240
 Leu Ser Arg Val Pro Glu Ile Glu Asp Met Glu Ile Ser Leu Pro Asn
 245 250 255
 Ile His Tyr Phe Asn Ile Asp Met Ser Lys Met Gly Leu Ile Asn Lys

260	265	270
Glu Glu Val Leu Leu Pro Leu Asp Asn Pro Tyr Gly Lys Ile Thr Gly		
275	280	285
Thr Val Lys Arg Lys Leu Ser Ser Arg Leu		
290	295	

<210> 9
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 <213> Artificial Sequence

<220>
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 20 25 30
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 35 40 45
 Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp
 50 55 60
 Val Ile Pro Thr Asp Thr Ile Lys Asn Thr Val Asn Val Leu Ala Lys
 65 70 75 80
 Phe Lys Gly Ile Lys Ser Ile Glu Thr Phe Ala Val Thr Ile Cys Glu
 85 90 95
 His Phe Leu Ser Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val
 100 105 110
 Glu Glu Val Pro Trp Lys Arg Phe Glu Lys Asn Gly Val Lys His Val
 115 120 125
 His Ala Phe Ile Tyr Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu
 130 135 140
 Gln Ile Arg Asn Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu
 145 150 155 160
 Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp
 165 170 175
 Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln
 180 185 190
 Val Tyr Cys Lys Trp Arg Tyr His Gln Gly Arg Asp Val Asp Phe Glu
 195 200 205
 Ala Thr Trp Asp Thr Val Arg Ser Ile Val Leu Gln Lys Phe Ala Gly
 210 215 220
 Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr
 225 230 235 240
 Asp Ile Gln Val Leu Ser Leu Ser Arg Val Pro Glu Ile Glu Asp Met

	245		250		255
Glu Ile Ser Leu Pro Asn Ile His Tyr Phe Asn Ile Asp Met Ser Lys	260		265		270
Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro	275		280		285
Tyr Gly Lys Ile Thr Gly Thr Val Lys Arg Lys Leu Ser	290		295		300

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 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PKS carboxy truncated

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 Lys Asp Met Ile Lys Val Leu His Ile Gln Arg Asp Gly Lys Tyr His
 20 25 30
 Ser Ile Lys Glu Val Ala Thr Ser Val Gln Leu Thr Leu Ser Ser Lys
 35 40 45
 Lys Asp Tyr Leu His Gly Asp Asn Ser Asp Val Ile Pro Thr Asp Thr
 50 55 60
 Ile Lys Asn Thr Val Asn Val Leu Ala Lys Phe Lys Gly Ile Lys Ser
 65 70 75 80
 Ile Glu Thr Phe Ala Val Thr Ile Cys Glu His Phe Leu Ser Ser Phe
 85 90 95
 Lys His Val Ile Arg Ala Gln Val Tyr Val Glu Glu Val Pro Trp Lys
 100 105 110
 Arg Phe Glu Lys Asn Gly Val Lys His Val His Ala Phe Ile Tyr Thr
 115 120 125
 Pro Thr Gly Thr His Phe Cys Glu Val Glu Gln Ile Arg Asn Gly Pro
 130 135 140
 Pro Val Ile His Ser Gly Ile Lys Asp Leu Lys Val Leu Lys Thr Thr
 145 150 155 160
 Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp Gln Phe Thr Thr Leu Pro
 165 170 175
 Glu Val Lys Asp Arg Cys Phe Ala Thr Gln Val Tyr Cys Lys Trp Arg
 180 185 190
 Tyr His Gln Gly Arg Asp Val Asp Phe Glu Ala Thr Trp Asp Thr Val
 195 200 205
 Arg Ser Ile Val Leu Gln Lys Phe Ala Gly Pro Tyr Asp Lys Gly Glu
 210 215 220
 Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr Asp Ile Gln Val Leu Thr

225		230		235		240
Leu Gly Gln Val	Pro Glu Ile Glu Asp	Met Glu Ile Ser Leu	Pro Asn			
	245		250			255
Ile His Tyr Leu	Asn Ile Asp Met Ser	Lys Met Gly Leu	Ile Asn Lys			
	260		265			270
Glu Glu Val Leu	Leu Pro Leu Asp Asn	Pro Tyr Gly Lys	Ile Thr Gly			
	275		280			285
Thr Val Lys Arg	Lys Leu Ser Ser	Arg Leu				
	290		295			

<210> 11
 <211> 301
 <212> PRT
 <213> Artificial Sequence

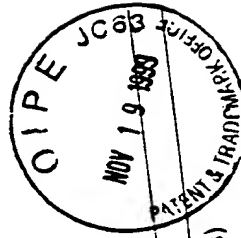
<220>
 <223> Description of Artificial Sequence:PKS carboxy truncated

<400> 11
 Met Ala His Tyr Arg Asn Asp Tyr Lys Lys Asn Asp Glu Val Glu Phe
 1 5 10 15
 Val Arg Thr Gly Tyr Gly Lys Asp Met Ile Lys Val Leu His Ile Gln
 20 25 30
 Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln
 35 40 45
 Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp
 50 55 60
 Val Ile Pro Thr Asp Thr Ile Lys Asn Thr Val Asn Val Leu Ala Lys
 65 70 75 80
 Phe Lys Gly Ile Lys Ser Ile Glu Thr Phe Ala Val Thr Ile Cys Glu
 85 90 95
 His Phe Leu Ser Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val
 100 105 110
 Glu Glu Val Pro Trp Lys Arg Phe Glu Lys Asn Gly Val Lys His Val
 115 120 125
 His Ala Phe Ile Tyr Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu
 130 135 140
 Gln Ile Arg Asn Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu
 145 150 155 160
 Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp
 165 170 175
 Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln
 180 185 190
 Val Tyr Cys Lys Trp Arg Tyr His Gln Gly Arg Asp Val Asp Phe Glu
 195 200 205

Ala	Thr	Trp	Asp	Thr	Val	Arg	Ser	Ile	Val	Leu	Gln	Lys	Phe	Ala	Gly
210						215					220				
Pro	Tyr	Asp	Lys	Gly	Glu	Tyr	Ser	Pro	Ser	Val	Gln	Lys	Thr	Leu	Tyr
225					230					235					240
Asp	Ile	Gln	Val	Leu	Thr	Leu	Gly	Gln	Val	Pro	Glu	Ile	Glu	Asp	Met
				245					250					255	
Glu	Ile	Ser	Leu	Pro	Asn	Ile	His	Tyr	Leu	Asn	Ile	Asp	Met	Ser	Lys
			260					265					270		
Met	Gly	Leu	Ile	Asn	Lys	Glu	Glu	Val	Leu	Leu	Pro	Leu	Asp	Asn	Pro
	275						280					285			
Tyr	Gly	Lys	Ile	Thr	Gly	Thr	Val	Lys	Arg	Lys	Leu	Ser			
290						295					300				

Atty: BJS
Date: 11-19-99
Client: 1579-379
Ref: 1579-379

Serial No.: PCT US99/17678
Applicant: Duke University
Title: PCT US99/17678



Amendment
Pages Specification
Claims
Sheets Drawings: Formal _____
Informal _____ Pages)
Declaration (_____ Pages)
Assignment
Priority Document
Base Issue Fee Transmittal
Fee (Check) _____

pages 37-49

Sequence Listing
Other: Disk (3.5")

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IN THE UNITED STATES RECEIVING OFFICE (RO/US)

BOX PCT

COPY

In re International Patent Application of

DUKE UNIVERSITY ET AL

Agent's File Ref: 1579-379

International Application No: **PCT/US99/17678**

International Filing Date: 05 August 1999

For: URATE OXIDASE

19 November 1999

United States Receiving Office
Honorable Commissioner of Patents
and Trademarks
Washington, D.C. 20231

Response to Correct Defects in International Application

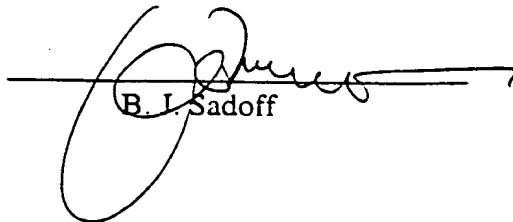
Dear Sirs,

Attached is a printed sequence listing for this application and a copy of the computer readable form on a 3.5" disk in the attached envelope.

In accordance with 37 CFR 1.821-1.825, I hereby state that the content of the paper and computer-readable copies of the sequence listing submitted in accordance with 37 CFR 1.821(c) and (e), respectively, are the same. I hereby state that the submission, filed in accordance with 37 CFR 1.821(g), does not introduce new matter.

Respectfully submitted,

NIXON & VANDERHYTE P.C.


B. J. Sadoff

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